SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: Lyman, Stewart D.

 Beckmann, M. Patricia
 - (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
 - (iii) NUMBER OF SEQUENCES: 8
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-C
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: $1..2\overline{5}$
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 855..879
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 57..752
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACTGGA A	ACGAGACGAC CI	TGCTCTGTC ACA	AGGCATGA	GGGGTCCCCG (GCAGAG 56
				TCC TCC CTG Ser Ser Leu	
				ACA CCT GAC Thr Pro Asp 30	
				GTG AAG TTT Val Lys Phe 45	
				ACT GTG GCC Thr Val Ala 60	
				AGC CTC TTC Ser Leu Phe	
				GGG TCT AAG Gly Ser Lys	
				TTT GTC ACC Phe Val Thr 110	
				GTC CAG ACC Val Gln Thr 125	

														AAG Lys		488
_						-								GTG Val		536
												_		ATA Ile 175		584
														TTG Leu		632
														GCC Ala		680
	_			_			_				-			CCT Pro		728
		CTC Leu					TAGO	GATT(CGA (GCCT'	rgtgo	CA TO	CGTT(GACT(779
AGC	CAGGO	GTC :	TATO	CTCG	ST TA	ACAC	CTGT	A ATO	CTCAC	GCCC	TTG	GGAG	CCC 2	AGAGO	CAGGAT	839
TGC	rgaa:	rgg :	rctgo	GAGC	AG G	CGT	CTCG:	r TC	CAGT	CGAC						879

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu 1 5 10 15

Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr 20 25 30

Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu 35 40 45

Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn 50 55 60

Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala 65 70 75 80

Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln 85 90 95

Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys 100 105 110

Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile 115 120 125

Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro 130 135 140

Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln 145 150 155 160

Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala 165 170 175

Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu 180 185 190

Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Trp
195 200 205

Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly 210 215 220

Val Pro Leu Pro Ser His Pro 225 230

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	(xi)	SEOUENCE	DESCRIPTION:	SEO	ID	NO:4
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AGCAGGTCGT CTCGTTCCAG	20
(2) INFORMATION FOR SEQ ID NO:5:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 988 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA to mRNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 30734	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
CGGCCGGAAT TCCGGGGCCC CCGGCCGAA ATG ACA GTG CTG GCG CCA GCC TGG Met Thr Val Leu Ala Pro Ala Trp 1 5	53
AGC CCA ACA ACC TAT CTC CTC CTG CTG CTG CTG CTG AGC TCG GGA CTC Ser Pro Thr Thr Tyr Leu Leu Leu Leu Leu Leu Leu Ser Ser Gly Leu 10 15 20	101
AGT GGG ACC CAG GAC TGC TCC TTC CAA CAC AGC CCC ATC TCC TCC GAC Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp 30 35 40	149
TTC GCT GTC AAA ATC CGT GAG CTG TCT GAC TAC CTG CTT CAA GAT TAC Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr 45	197
CCA GTC ACC GTG GCC TCC AAC CTG CAG GAC GAG GAG CTC TGC GGG GGC Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly 60 65 70	245
CTC TGG CGG CTG GTC CTG GCA CAG CGC TGG ATG GAG CGG CTC AAG ACT Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr 75 80 85	293
GTC GCT GGG TCC AAG ATG CAA GGC TTG CTG GAG CGC GTG AAC ACG GAG Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu 90 95 100	341
ATA CAC TTT GTC ACC AAA TGT GCC TTT CAG CCC CCC CCC AGC TGT CTT Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu 105	389
CGC TTC GTC CAG ACC AAC ATC TCC CGC CTC CTG CAG GAG ACC TCC GAG Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu 125	437

														TCC Ser		485
														CCC Pro		533
														CAG Gln		581
			-	_	-	-								CTG Leu		629
														CCC Pro 215		677
														CTG Leu		725
	GAG Glu		TGAG	CCTG	GCC 1	AAGGO	CCTC	AT CO	CTGC	GGAG	C CT	ГАААС	CAAC			774
GCA	GTGAC	SAC A	AGAC	ATCTA	AT CA	ATCC	CATT	TAC	CAGG	GGAG	GATA	ACTG	AGG (CACAC	CAGAGG	834
GGA	GTCA	CCA	GCCA	GAGG	AT G	CATAC	GCCTC	G GAG	CACAC	GAGG	AAG:	rTGG(CTA (GAGG	CCGGTC	894
CCT	CCT	rgg (SCCC	CTCT	CA TI	rccci	rccc	AG/	AATGO	GAGG	CAA	CGCCZ	AGA A	ATCC	AGCACC	954
GGC	CCCAT	TTT A	ACCC	AACTO	CT GA	AACAA	AAGCO	c ccc	CG							988

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu 1 5 10 15

Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe 20 25 30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu 35 40 45

Ser Asp Tyr Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu 50 60

Gln 65	Asp	Glu	Glu	Leu	Cys 70	Gly	Gly	Leu	Trp	Arg 75	Leu	Val	Leu	Ala	Gln 80	
Arg	Trp	Met	Glu	Arg 85	Leu	Lys	Thr	Val	Ala 90	Gly	Ser	Lys	Met	Gln 95	Gly	
Leu	Leu	Glu	Arg 100	Val	Asn	Thr	Glu	Ile 105	His	Phe	Val	Thr	Lys 110	Cys	Ala	
Phe	Gln	Pro 115	Pro	Pro	Ser	Cys	Leu 120	Arg	Phe	Val	Gln	Thr 125	Asn	Ile	Ser	
Arg	Leu 130	Leu	Gln	Glu	Thr	Ser 135	Glu	Gln	Leu	Val	Ala 140	Leu	Lys	Pro	Trp	
Ile 145	Thr	Arg	Gln	Asn	Phe 150	Ser	Arg	Cys	Leu	Glu 155	Leu	Gln	Суз	Gln	Pro 160	
Asp	Ser	Ser	Thr	Leu 165	Pro	Pro	Pro	Trp	Ser 170	Pro	Arg	Pro	Leu	Glu 175	Ala	
Thr	Ala	Pro	Thr 180	Ala	Pro	Gln	Pro	Pro 185	Leu	Leu	Leu	Leu	Leu 190	Leu	Leu	
Pro	Val	Gly 195	Leu	Leu	Leu	Leu	Ala 200	Ala	Ala	Trp	Суз	Leu 205	His	Trp	Gln	
Arg	Thr 210	Arg	Arg	Arg	Thr	Pro 215	Arg	Pro	Gly	Glu	Gln 220	Val	Pro	Pro	Val	
Pro 225	Ser	Pro	Gln	Asp	Leu 230	Leu	Leu	Val	Glu	His 235						
(2)	INF	ORMA!	TION	FOR	SEQ	ID I	10:7	:								
	(i)	() ()	A) Li B) Ti C) S'	ENGTI YPE: PRANI	HARAG H: 7: nuc: DEDNI DGY:	l ba: leic ESS:	se pa acio sino	airs d								
	(ii)) MO	LECU	LE T	YPE:	cDN	A to	mRN.	A							
	(iii)	HY	РОТНІ	ETIC	AL: 1	NO.										
	(iv) AN'	TI-S	ENSE	: NO											
	(xi) SE	QUEN	CE D	ESCR:	IPTI	ON:	SEQ	ID N	0:7:						
AAT	TGGT	ACC '	TTTG	GATA.	AA A	GAGA	CTAC	a ag	GACG.	ACGA	TGA	CAAG.	ACA	CCTG.	ACTGTT	60
ACT	TCAG	CCA (С													71

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
 ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37

TRADEMARK

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lyman, Stewart D.

 Beckmann, M. Patricia
- (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
- (iii) NUMBER OF SEQUENCES: 8
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-C
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..25

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 855..879

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACTGGA ACGAGAC	CGAC CTGCTCTGTC ACA	AGGCATGA GGGGTCCCCG GCAGAG	56
Met Thr Val Leu Al		CCA AAT TCC TCC CTG TTG CTG Pro Asn Ser Ser Leu Leu Leu 10 15	104
		CGG GGG ACA CCT GAC TGT TAC Arg Gly Thr Pro Asp Cys Tyr 30	152
TTC AGC CAC AGT CO	CC ATC TCC TCC AAC	TTC AAA GTG AAG TTT AGA GAG Phe Lys Val Lys Phe Arg Glu 45	200
		CCA GTC ACT GTG GCC GTC AAT Pro Val Thr Val Ala Val Asn 60	248
		TTG TGG AGC CTC TTC CTA GCC Leu Trp Ser Leu Phe Leu Ala 75 80	296
	lu Gln Leu Lys Thr	GTG GCA GGG TCT AAG ATG CAA Val Ala Gly Ser Lys Met Gln 90 95	344
		ATA CAT TTT GTC ACC TCA TGT Ile His Phe Val Thr Ser Cys 110	392
		G CGA TTC GTC CAG ACC AAC ATC Arg Phe Val Gln Thr Asn Ile 125	440
		CAG CTG CTT GCT CTG AAG CCC Gln Leu Leu Ala Leu Lys Pro 140	488

				GCC Ala												536
				TCC Ser 165												584
				GAG Glu												632
				CTG Leu												680
				CAA Gln												728
				TCC Ser			TAGO	GATT(CGA (GCCT	rgtg(CA TO	CGTT	GACTO	C	779
AGC	CAGG	GTC 1	TAT	CTCGC	GT TA	ACAC	CTGT	A ATO	CTCA	SCCC	TTG	GGAG	CCC I	AGAG	CAGGAT	839
TGC	rgaa 1	rgg 1	CTG	GAGCA	AG G	CGT	CTCG	r TCC	CAGT	CGAC						879
(2)	INF	ORMA	rion	FOR	SEQ	ID 1	10:2	:								
		(i) S	(A)	ENCE LEN TYPE TOPE	NGTH:	: 231 amino	l ami	ino a id		5						
	(:	ii) N	OLE	CULE	TYPE	E: p	rotei	in								
	(2	ki) S	SEQUE	ENCE	DESC	CRIP	rion:	: SE	Q ID	NO:2	2:					
Met 1	Thr	Val	Leu	Ala 5	Pro	Ala	Trp	Ser	Pro 10	Asn	Ser	Ser	Leu	Leu 15	Leu	
Leu	Leu	Leu	Leu 20	Leu	Ser	Pro	Cys	Leu 25	Arg	Gly	Thr	Pro	Asp 30	Cys	Tyr	
Phe	Ser	His 35	Ser	Pro	Ile	Ser	Ser 40	Asn	Phe	Lys	Val	Lys 45	Phe	Arg	Glu	
Leu	Thr 50	Asp	His	Leu	Leu	Lys 55	Asp	Tyr	Pro	Val	Thr 60	Val	Ala	Val	Asn	
Leu 65	Gln	Asp	Glu	Lys	His 70	Cys	Lys	Ala	Leu	Trp 75	Ser	Leu	Phe	Leu	Ala 80	
Gln	Arg	Trp	Ile	Glu 85	Gln	Leu	Lys	Thr	Val 90	Ala	Gly	Ser	Lys	Met 95	Gln	
Thr	Leu	Leu	Glu 100	Asp	Val	Asn	Thr	Glu 105	Ile	His	Phe	Val	Thr 110	Ser	Cys	



Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro 130 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln 150 155 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Trp 200 Gly Leu Arg Trp Gln Arg Ala Arg Arg Gly Glu Leu His Pro Gly 215 220 Val Pro Leu Pro Ser His Pro 225 230 (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: TCGACTGGAA CGAGACGACC TGCT 24 (2) INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: AGCAGGTCGT CTCGTTCCAG 20 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 988 base pairs

Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile 115 120 125

((iii)	HYF	отне	TICA	L: N	10								
	(iv)	ANT	I-SE	ENSE:	NO									
	(ix)	(P	TURE A) NA B) LO	ME/F			734							
	(xi)	SEC	UENC	CE DE	SCRI	PTIC	on: S	SEQ 1	D NO):5:				
CGGC	CCGGA	AT I	CCGG	GGCC	cc cc	CGGCC	GAA					CCA Pro		53
	CCA Pro 10													101
	GGG Gly													149
	GCT Ala													197
	GTC Val													245
	TGG Trp													293
	GCT Ala 90													341
	CAC His													389
	TTC Phe													437
	CTG Leu													485
	CTG Leu													533

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

				CCC Pro												581
				CTA Leu												629
				CTG Leu 205												677
			_	GTG Val			_									725
	GAG Glu		TGAC	CCTGC	GCC A	AAGGO	CTC	AT CC	CTGCC	GGAGC	CT1)AAA	CAAC			774
GCAC	GTGAC	SAC A	AGACA	ATCT	AT C	ATCC	CATTI	TAC	CAGGO	GAG	GATA	ACTG	AGG (CACAC	CAGAGG	834
GGAC	STCAC	CCA (GCCAC	GAGGA	AT GI	CATAC	GCCTC	GAC	CACAC	GAGG	AAG	TGG	CTA (GAGG	CCGGTC	894
CCTT	CCTI	rgg (CCCC	CTCTC	CA TI	rccci	rccc	AGA	AATGO	GAGG	CAAC	CGCCI	AGA A	ATCC	AGCACC	954
GGC	CCCAT	TTT A	ACCC	AACTO	CT GA	AACA	AAGC	ccc	CG							988
(2)	INFO	ORMA	rion	FOR	SEQ	ID 1	10:6:	:								
		(i) S	SEOUE	ENCE	СНАТ	א כיתינ	* T C T	17.00								
			(A)	LEN TYP	NGTH:	235 amino	ami aci	no a		3						-
	(i)		(A) (B) (D)	LEN TYP	IGTH: PE: & POLOG	: 235 amino GY: 1	ami aci	no a d		3						
		Li) N	(A) (B) (D)	LEN TYP TOP	GTH: PE: 6 POLOC	: 235 amino GY:]	ami aci linea	no a d ar n	acids		5:					
Met 1	(2	li) N ki) S	(A) (B) (D) (D)	LEN TYP TOP	OTH: PE: 6 POLOG TYPE	235 amino GY: 1 E: pi	ami aci linea cotei	no a d ar n : SE(acids	NO:		Tyr	Leu	Leu 15	Leu	
1	(2 Thr	ii) N xi) S Val	(A) (B) (D) MOLE(SEQUE Leu	LENCE Ala	NGTH: PE: 6 POLOG TYPE DESG	: 235 amino GY: 1 E: pr CRIPT	ami aci linea cotei TION:	no a d ar n SEQ	Pro	NO:	Thr			15		
1 Leu	(2 Thr Leu	ii) M ki) S Val Leu	(A) (B) (D) MOLE(SEQUE Leu 20	LEN TYPE TOPE CULE ENCE Ala 5	NGTH: PE: 8 POLOG TYPE DESG Pro	: 235 amino GY: 1 E: pr CRIPT Ala Gly	o ami o aci linea rotei TION: Trp	no a d ar SE(Ser 25	Pro 10	NO: 6	Thr Gln	Asp	Cys 30	15 Ser	Phe	
1 Leu Gln	(2 Thr Leu His	Leu Ser 35	(A) (B) (D) MOLE(SEQUE Leu 20 Pro	LENCE CULE ENCE Ala 5	NGTH: PE: 8 POLOG TYPE DESG Pro Ser	235 amino GY: 1 E: pr CRIPT Ala Gly Ser	S ami D aci D aci Linea Tro Tro Leu Asp 40	no and and ar second se	Pro 10 Gly	NO:6 Thr Thr	Thr Gln Lys	Asp Ile 45	Cys 30 Arg	15 Ser Glu	Phe Leu	
1 Leu Gln Ser	Thr Leu His Asp	ii) M xi) S Val Leu Ser 35	(A) (B) (D) MOLE SEQUE Leu 20 Pro	LENCE Ala 5	Gln	235 amino GY: 1 E: pr CRIPT Ala Gly Ser Asp 55	o ami o aci inea rotei TION: Trp Leu Asp 40	no and ar	Pro 10 Gly Ala	NO: 6 Thr Thr Val	Thr Gln Lys Val	Asp Ile 45 Ala	Cys 30 Arg Ser	15 Ser Glu Asn	Phe Leu Leu	
1 Leu Gln Ser Gln 65	Thr Leu His Asp 50 Asp	Leu Ser 35 Tyr	(A) (B) (D) MOLEC SEQUE Leu 20 Pro Leu Glu	LENCE Ala 5 Ser Ile	TYPE DESC Pro Ser Gln Cys 70	E: processor Ala Asp 55 Gly	S amico acidines cotes c	no and ar	Pro 10 Gly Ala Val	NO:6 Thr Thr Val Thr Arg 75	Thr Gln Lys Val 60 Leu	Asp Ile 45 Ala Val	Cys 30 Arg Ser	15 Ser Glu Asn Ala	Phe Leu Leu Gln 80	

Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser 120 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp 130 135 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro 150 155 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu 180 185 Pro Val Gly Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln 200 Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val 215 Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His 230 (2) INFORMATION FOR SEQ ID NO:7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT 71 ACTTCAGCCA C (2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

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